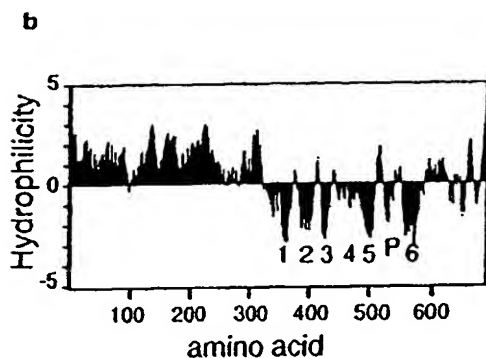


a

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GMFQQPYQQHGGFHHQNELQHLREFSDSHDNAFHHSYQQDRAGVSTLPN 100
NISHAYGGSHPLAESQHSGGPQSGPRIDPNHHPHQDDPHRPSEPLSHPS 150
TGSHQGTTHQQYHERSHHLNPQQNRDHADTISYRSSTRFYRSHAPFSRQE 200
RPHLHADHHHEGHHASHHGEHPHHKEQRHYHGDHMHIIHHRSPSASQL 250
SEGEDHVQKRKKAQRAHKAHTGNIFQLLWEKISHLLLGLQQMILSLTQS 350
      S1                                S2
LGFETFIFIIVCLNTVILVAQTFTELEIRGEWYFMVLDSIFLSIYVLEAV 400
      S3
LKLIALGLEFYDPWNNLDFFIMVMAVLDFVLLQINSISYSFYNHSLFRI 450
      S4                                S5
LKVFKSMRALRAIRVLRRLSILTSLEHVAGTSLGSLPSITAILTLMFTCL 500
      P
FLFSVVLRALFQDSDPKRFQNIFFTTLFTLFTMLTLDDWSLIYIDNRAQGA 550
      S6
WYIIIPILMIYIVIQYFIFLNLVIAVLVDNFQMAALLKGLEKVKLEQAARVH 600
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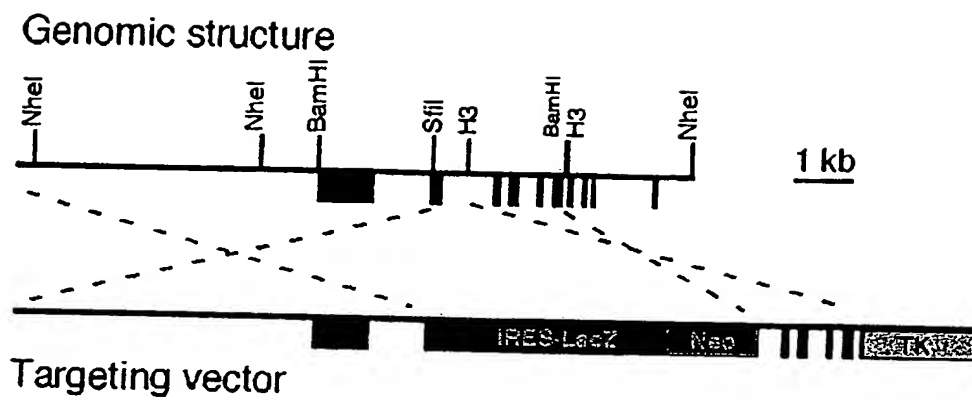


c

Pore region

CatSper	RFQNIFFTTLFTLFTMLTLDDWSLIYID
Cav1.2	NFDNFAFAMLTVFQCIIMGCTDVLN
I Cav2.2	NFDNLLFAILTVFQCIIMGCTDILN
Cav3.1	NFDNIGYAWIAIFQVITLGGVDIMYF
Cav1.2	TFDNFPQSLLTVFQILTGCDNSVMYD
II Cav2.2	NFDTFPAAILTVFQILTGCDNAVMYN
Cav3.1	NFDSLLWAIVTVFQILTGCDNKVLN
Cav1.2	DFDNVLAAMMAFTVSTFGCPPELLYR
III Cav2.2	HYDNVLWALLTLFTVSTFGCPHYLKH
Cav3.1	NFDNLGQALMSLFVLASKGCDVIMYD
Cav1.2	NFQTFPQAVLLLPKATGEAODIMLA
IV Cav2.2	NFRTFLQALMLLFRSATGEAHEIMLS
Cav3.1	TFRNFGMAFLTFRVSTGEAINGIMKD

FIG. 1

**FIG. 2**

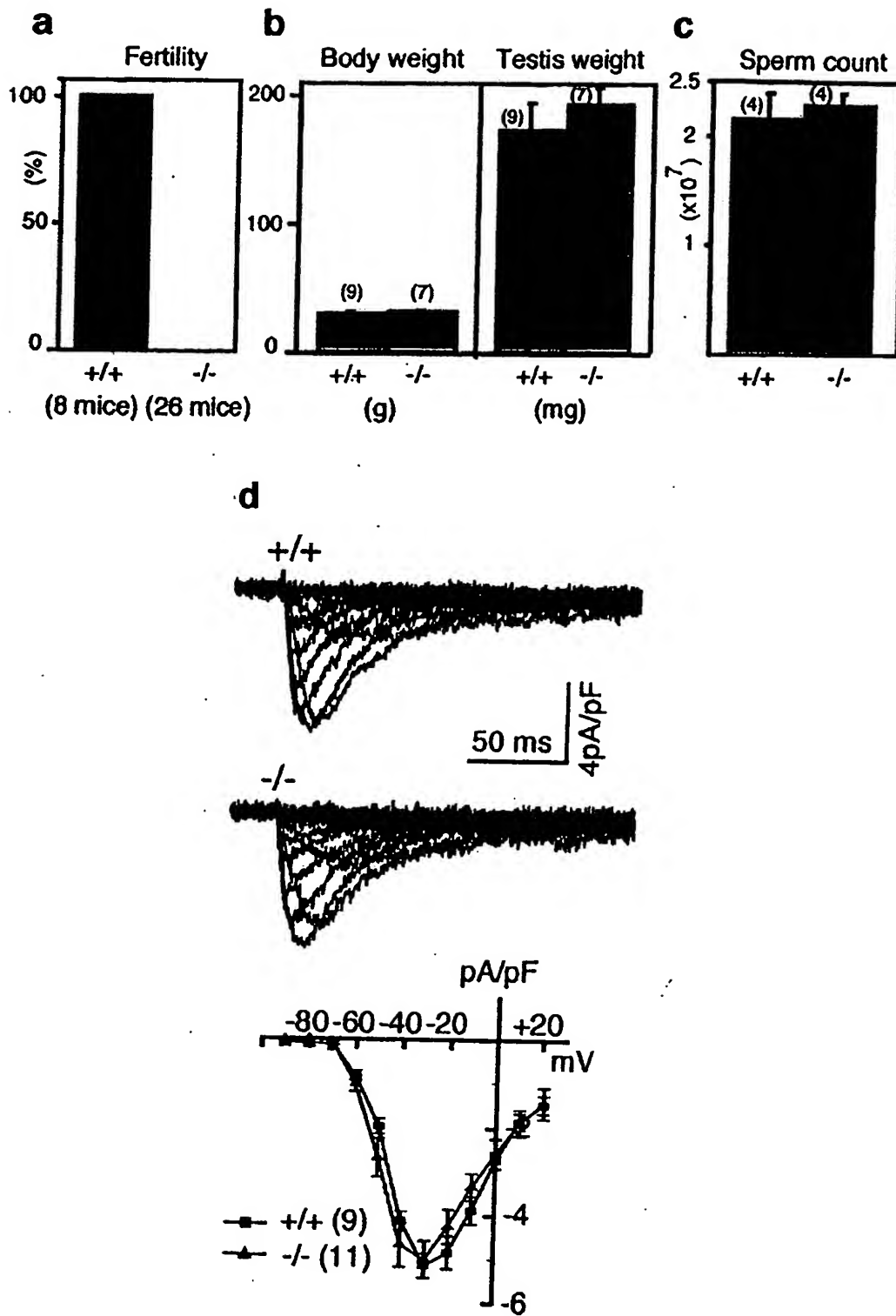


FIG. 3

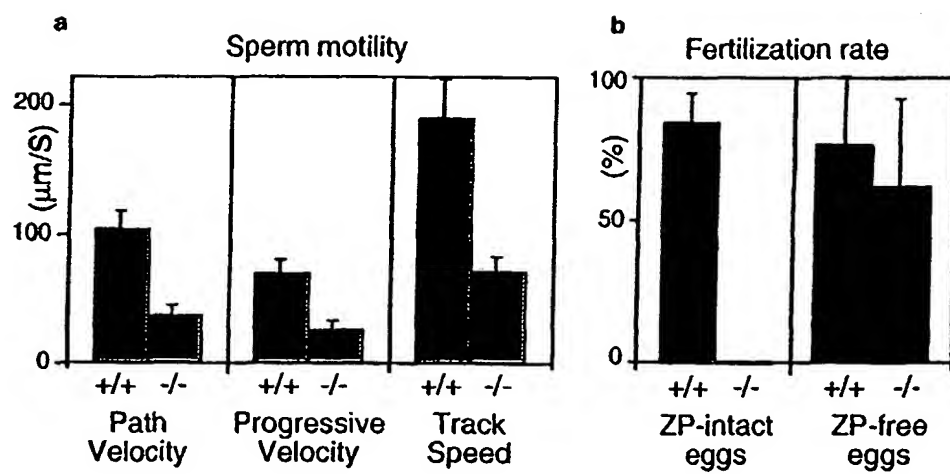


FIG. 4

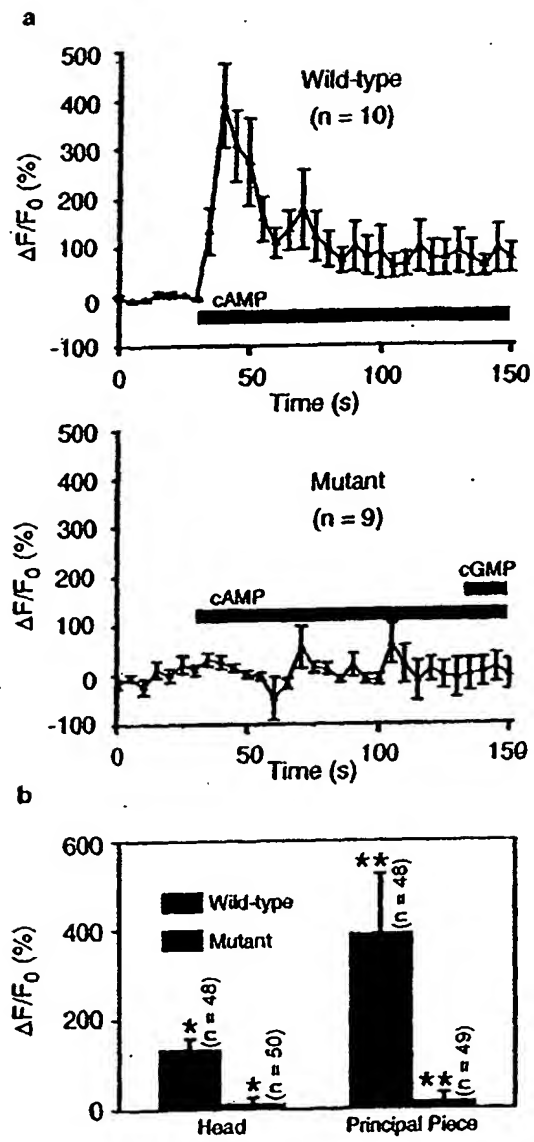


FIG. 5